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Draft Genome Sequence of *Mycobacterium arupense* Strain GUC1

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We report the draft genome sequence of *Mycobacterium arupense* strain GUC1 from a sputum sample of a patient with bronchiectasis. This is the first draft genome sequence of *Mycobacterium arupense*, a rapidly growing nonchromogenic mycobacteria.

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Mycobacterium arupense is a rapidly growing nonchromogenic mycobacteria that is closely related to the *Mycobacterium terrae* complex and has been isolated from clinical samples, most commonly sputum samples, as well as environmental water sources (1–3). Multiple reports of tenosynovitis and osteoarticular infections with *M. arupense* have also been presented, including infections caused by the type strain AR30097 (4–8). Although the unique identification of *M. arupense* has generally been related to sequence analysis, the phenotypic properties of *M. arupense* that resulted in it being classified as a species include its inability to grow at 42°C, rapid growth at 30°C, variable pyrazinamidase activity, and mycolic acid patterns that distinguish it from *M. terrae* (1).

Rapidly growing mycobacteria constitute a commonly isolated population of acid-fast bacillus in the clinical microbiology lab of varying clinical importance (9, 10). We sequenced the first draft genome of *M. arupense* from a sputum sample of a patient diagnosed with bronchiectasis. The isolate was originally typed as *M. terrae* complex by high-performance liquid chromatography; however, genome sequencing and analysis of the 16S and *rpoB* sequences revealed its identity as *M. arupense*.

DNA from *M. arupense* strain GUC1 was extracted using the Qiagen EZ1 kit, and paired-end libraries were prepared using the Nextera XT DNA library kit followed by sequencing on the Illumina MiSeq. Sequences were adapter and quality (Q20) trimmed using cutadapt, *de novo* assembled using SPAdes v3.5, metagenomically screened for contaminating sequence with SURPI, and annotated via prokka v1.1 (11–14). A total of 6,386,174 paired-end reads of average length 117 nucleotides were recovered after trimming. *De novo* assembly yielded 173 contigs for a total assembly size of 4,441,412 bp with an N_{50} of 56,189 bp, an average coverage of 115×, and a total of 4,182 coding sequences. Contiguity was most likely disrupted by the high G+C content (67%) along with several high-copy-number integrases, transposases, and recombinases that were longer than sequence read length. Other high-copy number contigs included those containing genes to ESX/type VII secretion system, a distantly related 3-methyladenine glycosylase, and a copper-transporting ATPase. The assembly also includes 44 kb across two contigs that aligns with 99 to 100% nucleotide identity to the pMK12478 plasmid from *Mycobacterium kansasii* strain ATCC 12478 (15). Otherwise, the closest aligning sequenced genomes were *Mycobacterium* sp. JDM601 or *Mycobacterium avium* strains E1/E93 at approximately 80% nucleotide identity. By Comprehensive Antibiotic Resistance Database analysis, the GUC1 strain includes an *ampC* beta-lactamase and two metallo-beta-lactamases which demonstrate 80%, 90%, and 77% amino acid identity to that of *M. avium* strain Env 77, respectively (16, 17).

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession no. LASW00000000. The assembly described in this paper is the second version, LASW02000000.

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